

FIGURE 1

	TCGGCAAAGC AGCCGGATAC CGCTAAGTAT CTTGAAGTAT TGAAATATT ACGATGCAAA	60
5	AAAGAAAATT TAAGTATAAT ACAGCAGGAT TCTTTAAGG ATTCTTAACA ATTTTCTTAA	120
	CTGACCATAA <u>AGGA</u> ACCAAA AT ATG AAA AAA GCA CTT GGC ACA CTG ATT GGC	172
	Met Lys Lys Ala Leu Ala <u>Thr</u> Leu Ile Ala	
10	-19 -15 -10	
	CTC GCT CTC CCG GCC GGC GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC	220
	Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Ser Gly Phe Tyr	
	-5 1 5	
15	GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA GGT TCT	268
	Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly Ser	
	10 15 20	
20	GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC	316
	Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp	
	25 30 35	
25	CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA GGC CCA	364
	Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys <u>Ala</u> Pro	
	40 45 50 55	
30	TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC	412
	Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp	
	60 65 70	
35	TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC	460
	Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser	
	75 80 85	
40	CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC AGC CAA	508
	Leu Asn Arg Ala Ser Val Asp <u>Leu</u> Gly Gly Ser Asp Ser Phe Ser Gln	
	90 95 100	
45	ACC TCC <u>ATC</u> GGC CTC GGC GTA TTG ACG GGC GTA AGC TAT GCC GTT ACC	556
	Thr Ser <u>Ile</u> Gly Leu Gly Val Leu <u>Thr</u> Gly Val Ser Tyr Ala Val Thr	
	105 110 115	
50	CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA	604
	Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys	
	120 125 130 135	
55	GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC <u>GTC</u> GGC GTG	652
	Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser <u>Val</u> Gly Val	
	140 145 150	
60	CGC GTC AAA TTC TGATATGGGC CTTATTCTGC AAACCGCGGA GCGTTGGGCG	704
	Arg Val Lys Phe	
	155	
65	GTITTTGTTTT CTGCCACCGC AACTACACAA GCGCGCGGTT TTGTACGATA ATCCCGAATG	764
	CTGCGGCTTC TCGCGCCCTA TTTTITGAGG AATCCGAAT GTCCAAAAC ATCATOCACA	824
	CCGACA	830

FIGURE 2

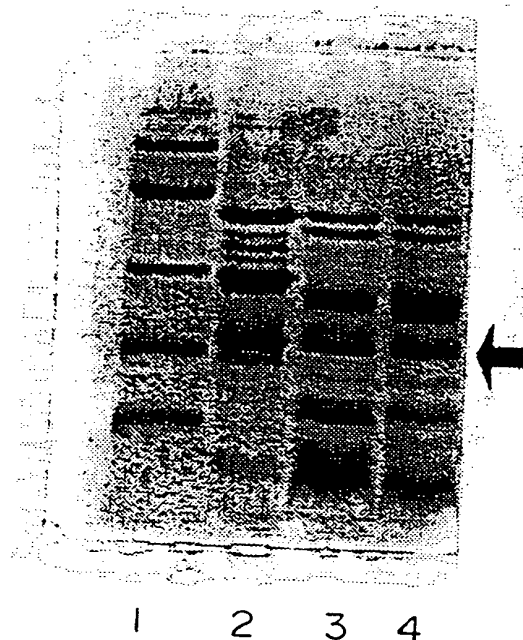


FIGURE 3a

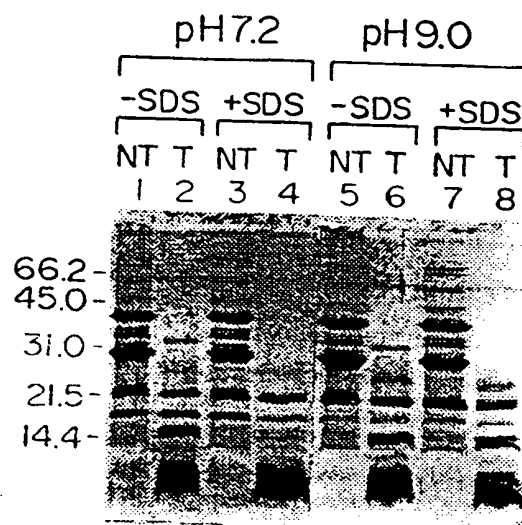


FIGURE 3b

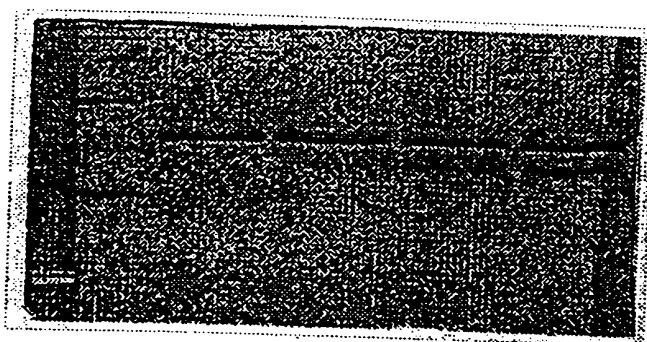
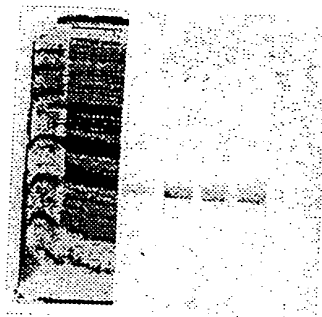
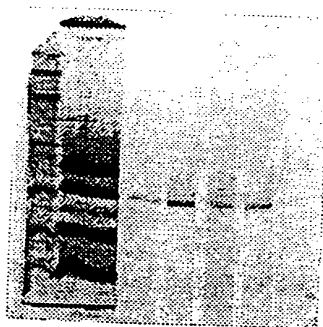


FIGURE 4a



1 2 3 4 5 6

FIGURE 4b



1 2 3 4 5 6

FIGURE 5

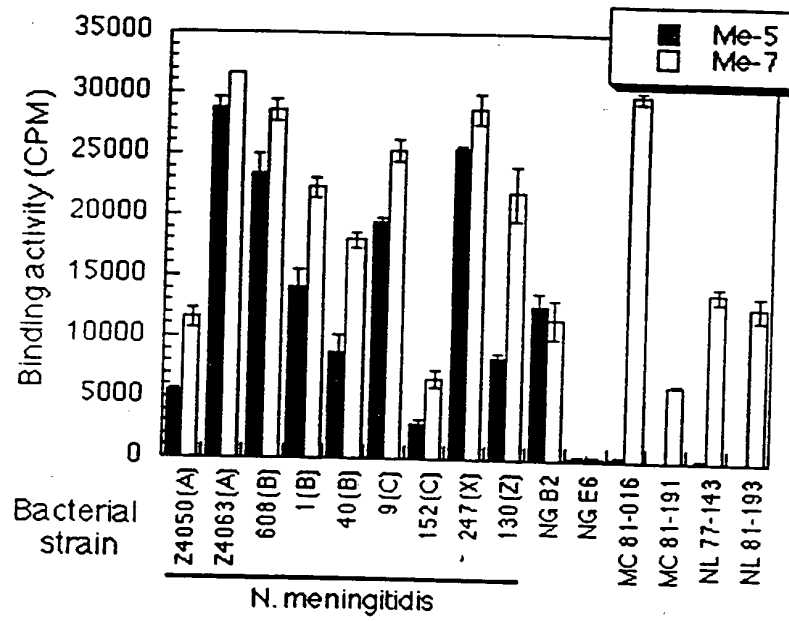
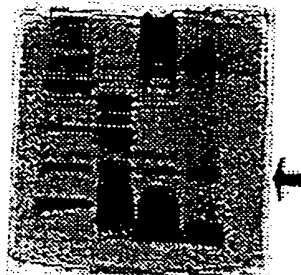
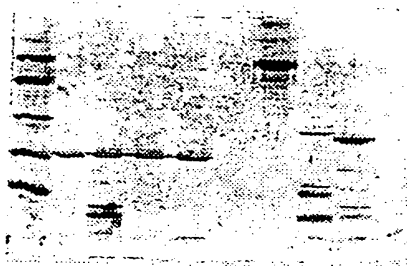


FIGURE 6A



1 2 3 4

FIGURE 6B



1 2 3 4 5 7 8 9 10

FIGURE 6C

NTCTK

005001-00010000

FIGURE 7

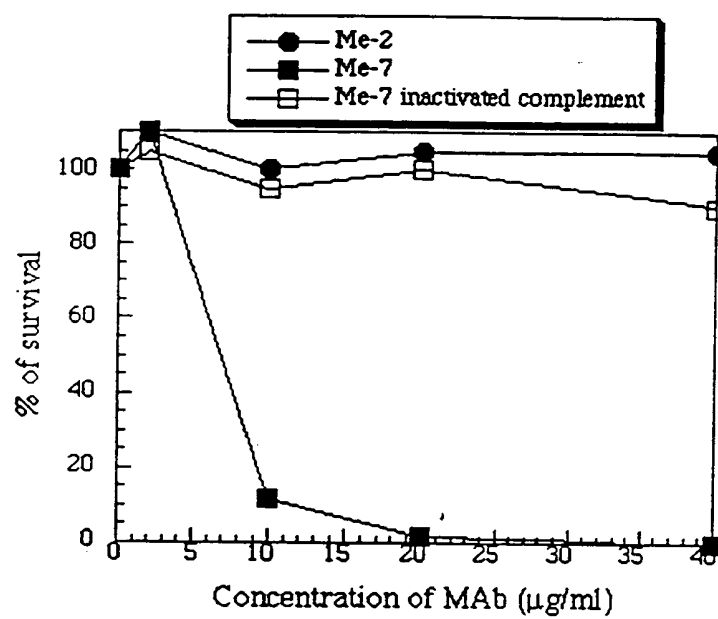


FIGURE 8

5	GTATCTTGAG GCATTGAAA TATTACAATG CAAAAGAAA ATTTCACTAT AATACGGCAG	60
	GATTCITTTAA CGGATTCCTTA ACCATTTTTC TCCCTGACCA TAAAGGAATC AAGAT ATG	118
		Met -19
10	AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCC CTC CCG GCC GCC GCA	166
	Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro-Ala Ala Ala	
	-15 -10 -5	
15	CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA CAC	214
	Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His	
	1 5 10	
20	GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG CGC	262
	Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg	
	15 20 25 30	
25	ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT TAC	310
	Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr	
	35 40 45	
30	ACG CGC TAC AAA AAC TAT AAA CAA GTC CCA TCC ACC GAT TTC AAA CTT	358
	Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu	
	50 55 60	
35	TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC TTC GAC ACC CAA TCC CCC	406
	Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro	
	65 70 75	
40	GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC CTC AAC CGC GCC TCC GTC	454
	Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser,Leu Asn Arg Ala Ser Val	
	80 85 90	
45	GAC TTT AAC GGC AGC GAC AGC TTC AGC CAA ACC TCC ACC GGC CTC GGC	502
	Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly	
	95 100 105 110	
50	GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT	550
	Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp	
	115 120 125	
55	GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA GTC AAC ACT GTC AAA AAT	598
	Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn	
	130 135 140	
60	GTC CGT TCC GGC GAA CTG TCC GCC GGC GTA CGC GTC AAA TTC TGATATACGC	650
	Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe	
	145 150 155	
65	GTTATTCCGC AAACCGCGCA GCCTTTCCGC GGTITTTTTC TCCGCGCGCG CAACTACACA	710

FIGURE 9

5	CACCCATCG CCGGTGATG CCGCCACCAC CATTAAAGG CAACGGCGG GITAACGGCT	60
	TTGCCGTGG CAAAGCAGCC GGATACCGCT ACGTATCTTG AAGTATTAAA AATATTACGA	120
	TGCAAAAAGA AAATTAAAGT ATAATAAAGC AGAATTCTTT AACGGATTCT TAACAATTTT	180
10	TCTAACTGAC CATAAAGGAA CCAAAAT ATG AAA AAA GCA CTT GCC ACA CTG	231
	Met Lys Lys Ala Leu Ala Thr Leu	
	-19 -15	
15	ATT GCC CTC GCT CTC CCG GCC GCC GCA CTG CCG GAA GGC GCA TCC GGC	279
	Ile Ala Leu Ala Leu Pro Ala Ala Leu Ala Glu Gly Ala Ser Gly	
	-10 -5 1 5	
20	TTT TAC GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA	327
	Phe Tyr Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu	
	10 15 20	
25	GGT TCT GCC AAA GGC TTC AGC CCG CCG ATC TCC GCA GGC TAC CGC ATC	375
	Gly Ser Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile	
	25 30 35	
30	AAC GAC CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA	423
	Asn Asp Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys	
	40 45 50	
35	GCC CCA TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT	471
	Ala Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile	
	55 60 65	
40	TAC GAC TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC	519
	Tyr Asp Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg	
	70 75 80 85	
45	TTG AGC CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC	567
	Leu Ser Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe	
	90 95 100	
50	AGC CAA ACC TCC ACC GGC CTC GGC GTA TTG GCG GGC GTA AGC TAT GCC	615
	Ser Gln Thr Ser Thr Gly Leu Gly Val Leu Ala Gly Val Ser Tyr Ala	
	105 110 115	
55	GTT ACC CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC	663
	Val Thr Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile	
	120 125 130	
60	GGC AAA GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GCC	711
	Gly Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Ala	
	135 140 145	
65	GGT GTG CGC GTC AAA TTC TGATATGGC CTTATTCTGC AAACCGCGA	759
	Gly Val Arg Val Lys Phe	
	150 155	
70	GCCTTGGCG GTTTGTGTTT CTGCCACGC AACTACACAA GCGGCGGTT TTGTACGATA	819
	ATCCCGAATG CTGCGGCTTC TGCGGCCCTA T	850

FIGURE 10

5	CCCCGCCCTTT GCGGTTTTTTT CCAAACCGTT TGCAAGTTTC ACCCATCCGC CGCGTGATGC	60
	CGCCGTTTAA GGGCAACGCG CGGGTTAAGC GATTGCGGT CGGCAAGCA GCGGATGCC	120
	GCCGCGTATC TTGAGGCATT GAAAATATTA CGATGCAAAA AGAAAATTTC AGTATAATAC	180
10	GGCAGGATTC TTTAACGGAT TATTAACAAT TTTTCTCCCT GACCATAAG GAACCAAAAT	240
	ATG AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCA CTC CCG GCC GCC	288
	Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala	
	-19 -15 -10 -5	
15	GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA	336
	Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala	
	1 5 10	
20	CAC GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG	384
	His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro	
	15 20 25	
25	CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT	432
	Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp	
	30 35 40 45	
30	TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA TCC ACC GAT TTC AAA CTT	480
	Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu	
	50 55 60	
35	TAC AGC ATC GGC GCG TCC GTC ATT TAC GAC TTC GAC ACC CAA TCG CCC	528
	Tyr Ser Ile Gly Ala Ser Val Ile Tyr Asp Phe Asp Thr Gln Ser Pro	
	65 70 75	
40	GTC AAA CCG TAT TTC GGC GCG CGC TTG AGC CTC AAC CGC GCT TCC GCC	576
	Val Lys Pro Tyr Phe Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Ala	
	80 85 90	
45	CAC TTG GGC GGC AGC GAC AGC TTC AGC AAA ACC TCC GCC GGC CTC GGC	624
	His Leu Gly Gly Ser Asp Ser Phe Ser Lys Thr Ser Ala Gly Leu Gly	
	95 100 105	
50	GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT	672
	Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp	
	110 115 120 125	
55	GCC GGC TAC CGC TAC AAC TAC GTC GGC AAA GTC AAC ACT GTC AAA AAC	720
	Ala Gly Tyr Arg Tyr Asn Tyr Val Gly Lys Val Asn Thr Val Lys Asn	
	130 135 140	
60	GTC CGT TCC GGC GAA CTG TCC GCC GGC GTG CGC GTC AAA TTC TGATATACGC	772
	Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe	
	145 150 155	
65	GTTATTCCGC AAACCGCGCA GCCTTCGGCG GTTTTTTG	810

FIGURE 11

5	MCH88-ORFG.C.....	50	
	608B-ORFA.T.....	50	
	Z4063-ORFA.T.....	50	
	gono b2-ORFG.A.....	50	
	Consensus	ATGAAAAAAG	CACCTTGCCRC	ACTGATTGCC	CTCGCHCTCC	CGGCCGCCGC
10	MCH88-ORF	100
	608B-ORF	100
	Z4063-ORF	100
	gono b2-ORF	100
	Consensus	ACTGGCGGAA	GGCGCATCCG	GCTTTTACGT	CCAAGCCGAT	GCCGCACACG
15	MCH88-ORF	.C.....	150
	608B-ORF	.A.....	150
	Z4063-ORF	.A.....	150
	gono b2-ORF	.C.....	150
	Consensus	CHAAAGCCTC	AAGCTCTTTA	GGTTCTGCCA	AAGGCTTCAG	CCCGCGCATC
20	MCH88-ORF	200
	608B-ORF	200
	Z4063-ORF	200
	gono b2-ORF	200
	Consensus	TCCGCAGGCT	ACCGCATCAA	CGACCTCCGC	TTGCGCGTCG	ATTACACGCG
25	MCH88-ORF	250
	608B-ORF	247
	Z4063-ORF	247
	gono b2-ORF	247
	Consensus	CTACAAAAAC	TATAAACAAG	YCCCATCCAC	CGATTTCAAA	CTTTACAGCA
30	MCH88-ORF	300
	608B-ORF	297
	Z4063-ORF	297
	gono b2-ORF	297
	Consensus	TCCGCGCGTC	CGYCATTTAC	GACTTCGACA	CCCAATCSCC	CGTCAAACCG
35	MCH88-ORF	350
	608B-ORF	347
	Z4063-ORF	347
	gono b2-ORF	347
	Consensus	TATYTCGGCG	CGCGCTGAG	CCTCAACCGC	GCTTCGCGTA	TTGRCGGGCG
40	MCH88-ORF	400
	608B-ORF	397
	Z4063-ORF	397
	gono b2-ORF	397
	Consensus	CAGCGACAGC	TTCAGCHAAA	CCTCCRYCGG	CCTCGGCGTA	TTGRCGGGCG
45	MCH88-ORF	450
	608B-ORF	447
	Z4063-ORF	447
	gono b2-ORF	447
	Consensus	TAAGCTATGC	CGTTACCCCG	AATGTCGATT	TGGATGCCGG	CTACCGCTAC
50	MCH88-ORF	500
	608B-ORF	497
	Z4063-ORF	497
	gono b2-ORF	497
	Consensus	AACCTACRTCG	GCAAAGTCAA	CACGTGTCAA	AAYGTCCGTT	CCGGCGAACT
55	MCH88-ORF	528
	608B-ORF	525
	Z4063-ORF	525
	gono b2-ORF	525
	Consensus	GTCGCGCGY	GTRCGCGTCA	AATTCCTGA

FIGURE 12

5	gonoB2A...	50
	Z4063T...	50
	608BT...	50
	MCH88A...	50
	Consensus	MKKALA.LIA	LALPAAALAE	GASGFYVQAD	AAHAKASSSL	GSAGFSPRI	50
10	gonoB2V..	99
	Z4063	99
	608B	99
	MCH88QV.....	99
	Consensus	SAGYRINDLR	FAVDYTRYKN	YK-APSTDFK	LYSIGASAIY	DFDTQSPVKP	100
15	gonoB2	.F.....	..AH.....	..K..A....	149
	Z4063T....	149
	608BI....	..T.....	149
	MCH88FN....T....	150
	Consensus	YLGARLSLNR	ASVDLGGSDS	FSQTS.GLGV	LAGVSYAVTP	NVDLDAGYRY	150
20	gonoB2	..V.....	174
	Z4063	174
	608BV..	174
	MCH88	175
	Consensus	NYIGKVNTVK	NVRSGELSAG	VRVKF	175
25	gonoB2	175
	Z4063	175
	608B	175
	MCH88	175
	Consensus	NYIGKVNTVK	NVRSGELSAG	VRVKF	175

FIGURE 13

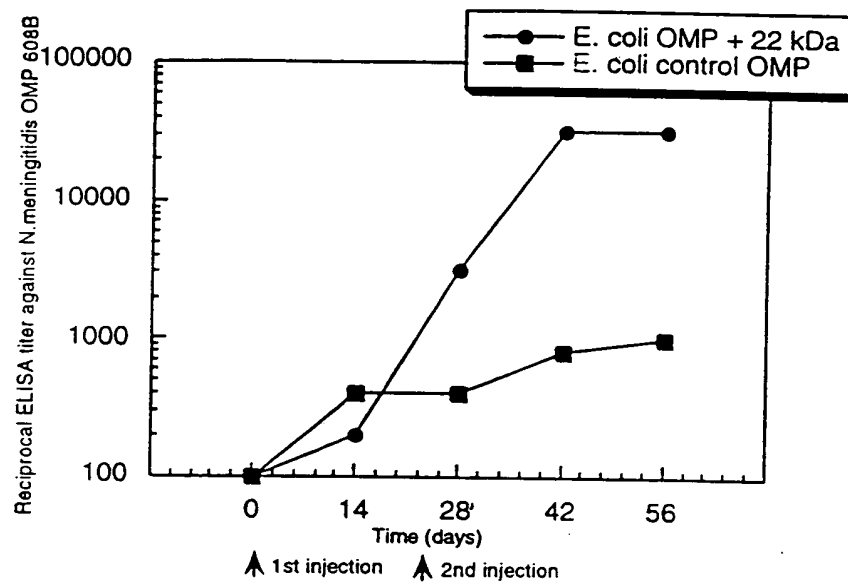


FIGURE 14

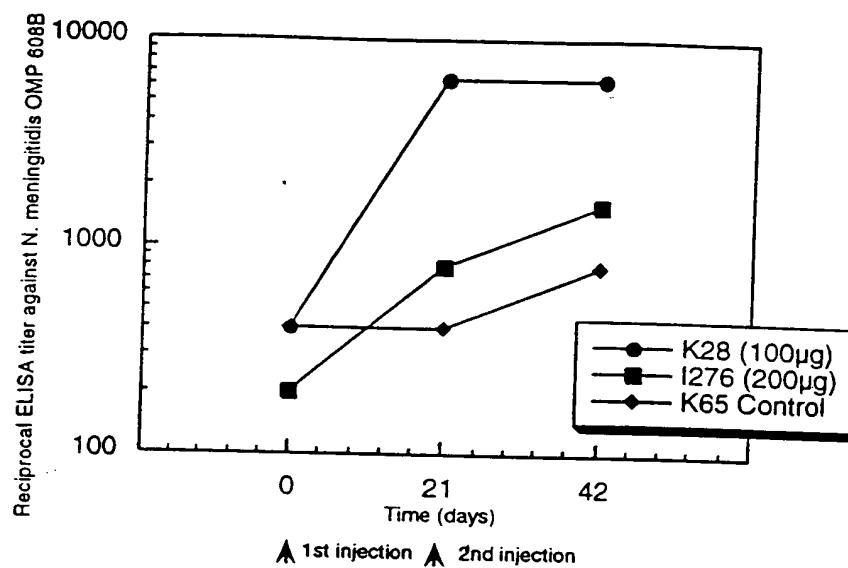


FIGURE 15

	MKKALATLIA	LALPAAALAE	GASGFYVQAD	AAHAKASSSL	GSAGFSPRI	50
5	CS-840		CS-842		CS-844	
		CS-841		CS-843		
10	SAGYRINDLR	FAVDYTRYKN	YKAPSTDFKL	YSIGASAIYD	FDTQSPVKPY	100
		CS-846		CS-848		
	CS-845		CS-847		CS-849	
15		CS-857				
	LGARLSLNRA	SVDLGGSDSF	SQTSIGLGVL	TGVSYAVTPN	VDLDAGYRYN	150
20	CS-850		CS-852		CS-854	
		CS-851		CS-853		
25	YIGKVNTVKN	VRSGELSVGV	RVKF			174
		CS-856				
	CS-855					
30						

FIGURE 16

